

**This Page Is Inserted by IFW Operations
and is not a part of the Official Record**

BEST AVAILABLE IMAGES

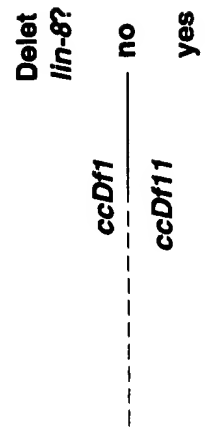
Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- **BLACK BORDERS**
- **TEXT CUT OFF AT TOP, BOTTOM OR SIDES**
- **FADED TEXT**
- **ILLEGIBLE TEXT**
- **SKEWED/SLANTED IMAGES**
- **COLORED PHOTOS**
- **BLACK OR VERY BLACK AND WHITE DARK PHOTOS**
- **GRAY SCALE DOCUMENTS**

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problems Mailbox.**

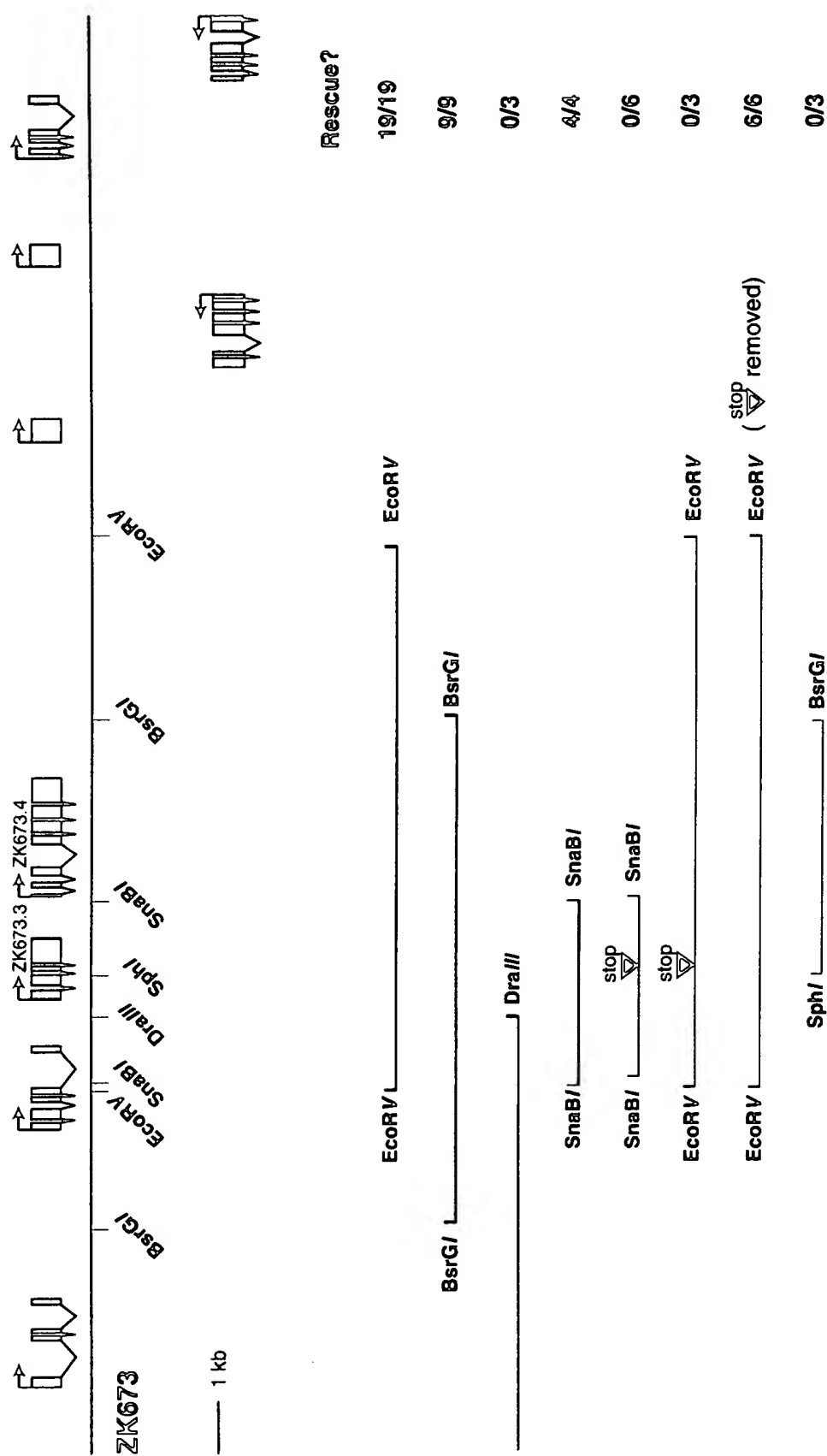
[illegible]

[illegible]

FIG. 3

	$\nabla n111p$	$\nabla n2741M$	
LIN-8	MSKIKTHSTGSKRTVPFYKLPBPVPLPPLPPPDPTRYFSTEKYIALSKDEKFKFDDYDVNDLTKKVVLENEIGKC		75
C41H7.3	MLSTKQE-----LLDAPBPBPAAATPLPPI--THRISLSGYRNI--HAKSFLKTMMDLCVRRVMSLLENR		62
C41H7.4	MSLKQE-----HMHPBPRAITPLPPA--THQITLFEYKER--EKDYRYRDATKDSVKKVMESLLKDH		60
C41H7.5	MSLKQE-----HMNPBPRTIITPLPPP--THQITIIEYKER--VKRDYRYRNATKDTSLKVVLSLIKDR		60
C41H7.6	MLNTKQE-----GVVADAPRALTIPIPF--IHVSMEEYMGMM--ELNSVYEEATKDSALKKVMLDLLKDR		61
C08A9.6	MMNPKEE--PRPFSIVPLPRPRPTTLPPI--SHCITMADYLL--ENTKFHKATRAPKIKKVLISLLKDR		67
C08A9.7	MVSATRV--PRRSSTTSATAQRTPSPLMPA--SFPITMDEYLEK--ENREFVUNASKDIAMKRLALTLELY		68
F14D2.2	MSRIKQE-----QVNPPPPRAITPLPPA--THRITMDEYKKR--EKKDYRYRDATKDSVKKVVLSLLKDY		62
		$\nabla n3585H$	
LIN-8	PDIWSSRSQAAMEHYPIVATETYRRITGLLL-----SIKSLKQIYKCGKDNLRNRLRVAIVSKRLTPAQVEAY		143
C41H7.3	RALWIRVHKSPKADWEVLGV-EVFERTGKAV-----SVKQLQRIFLTARDWLRRNLQLYIIQRKMDKLTLDAAE		129
C41H7.4	PGMWQNGNRFQPEKWRALGV-DVYQRTGQIV-----RVNDRMKMLVMGKSVLKKKIAICTRDKKLDRAAATEKD		127
C41H7.5	KAMWAPAAKPSDEKWKQLGA-EVFSRTGKVV-----SVTQLRRMLVSSKHVLKTKMSHCIVKVKMDRVSTEAY		134
C41H7.6	PGMWQNGNRFQLENWRELGV-DVYQRTGQIVRAELGEVSVDNMRMFVVGKAVKQKITVCTIRYKLDRAATEAD		128
C08A9.6	PEIWDRAKAQFSAKNWQNLGV-EVYERTGIYV-----RSNDLHKMLRTAKVVLKNKLRCTIGIKKLDRAATEE		134
C08A9.7	PEMWKPGGPMVAKKWQAFGA-EMYRRITGKIY-----RCKDLHSVFTLTSSIKRKLRTCTILIKRMHRSKTDEE		135
F14D2.2	PDMWQNGNRFQTRKWRALGV-EVYQRTGQIV-----GVDDMRKMFMSGKTVLKQKITFCIRNMKMDRAATEAD		129
	$\nabla n3648H$ $\nabla n2378K$ $\nabla n2378C$ $\nabla n2403K$ $\nabla n2724K$ $\nabla n3607K$		
LIN-8	MWRMEFYGFIRYRYRDYTORWEADLLKDLVDVLGLEARRASKNMEKVDSGELMEPMPMDSTMDMCVEEPP...		214
C41H7.3	LAKWELYPHFYIRYQYLGQFEAHL-----WTGELY-----DDIICDGMQVEV...		177
C41H7.4	LWYWEYRHFYRYRETLGQFEANL-----RGE-----WTGEDQIQDE--DDIYDGMLDGDL...		178
C41H7.5	LWNWEFYRHFYRYREMLDRFEANL-----RGKQ-----WTGEDQPTDD-DDIICDGMFEVEM...		186
C41H7.6	LQNWFEYRHFYRYRETLGQFEANL-----RGEQ-----WTGEDQADD-DDIYDGMFEVEM...		180
C08A9.6	LWKWEYYPHFYRYRETLGHFEANL-----RGE-----WDGEAHIDDD-DDDIYEGYWEADK...		186
C08A9.7	MWKYELYPYFQYRYRQSIGQFEAKL-----RDEP-----WTGEDQAQED--DDILFDGLFEVEN...		186
F14D2.2	LQNWEYRHFYRYRQTLGKFEAKL-----RGEQ-----WIGEDQVEDDEDVIFDGES		178
	$\nabla n3591K$		
LIN-8	...EEMNQITYQAIRIAREQPERLKLRLKALFDVVLAFDQK--EYADVGDLYRDLAQKNS		386
C41H7.3	...EDSVSYTKITEDLLQKKPHKHRFIRQALFKTIMALDDDEVEYTELADLFGDIAEQSNVVRRLRLQRQQQRGRGEQ		366
C41H7.4	...RSAQHIAEQAKRLFLQYPEKSNLIRETMFKTILAFDDPSADYQNVGEIFDDLAAQEAARKKRAENRAQREQQ		331
C41H7.5	...STAEQIGEEIDRLIQLYPQREMLIRQAFFKTIFALEDETVEFSNLGDLFEDLAEQENFKRRRRSRAQRLE		327
C41H7.6	...STAEQIGEEIDRLIQLYPQREMLIRQAFFKTIFALEDETVEFSNLGDLFEDLAEQENFKRRRRSRAQRLE		321
C08A9.6	...NSAQHIGEQVHRLFAQYPERSKLFRETLEKTIILALEEP--EYEHAEEVFTDLAQSETAKRRRRSEATWQNGQ		344
C08A9.7	...KTADNIGDQVKQLFVDHPDRANFFREVLFKTVLELRDP--AFTNAGVFFDEMSSLESAKRRRRSEMNK		331

FIG. 5



1000 999 998 997 996 995 994 993 992 991 990 989 988 987 986 985 984 983 982 981 980 979 978 977 976 975 974 973 972 971 970 969 968 967 966 965 964 963 962 961 960 959 958 957 956 955 954 953 952 951 950 949 948 947 946 945 944 943 942 941 940 939 938 937 936 935 934 933 932 931 930 929 928 927 926 925 924 923 922 921 920 919 918 917 916 915 914 913 912 911 910 909 908 907 906 905 904 903 902 901 900 899 898 897 896 895 894 893 892 891 890 889 888 887 886 885 884 883 882 881 880 879 878 877 876 875 874 873 872 871 870 869 868 867 866 865 864 863 862 861 860 859 858 857 856 855 854 853 852 851 850 849 848 847 846 845 844 843 842 841 840 839 838 837 836 835 834 833 832 831 830 829 828 827 826 825 824 823 822 821 820 819 818 817 816 815 814 813 812 811 810 809 808 807 806 805 804 803 802 801 800 799 798 797 796 795 794 793 792 791 790 789 788 787 786 785 784 783 782 781 780 779 778 777 776 775 774 773 772 771 770 769 768 767 766 765 764 763 762 761 760 759 758 757 756 755 754 753 752 751 750 749 748 747 746 745 744 743 742 741 740 739 738 737 736 735 734 733 732 731 730 729 728 727 726 725 724 723 722 721 720 719 718 717 716 715 714 713 712 711 710 709 708 707 706 705 704 703 702 701 700 699 698 697 696 695 694 693 692 691 690 689 688 687 686 685 684 683 682 681 680 679 678 677 676 675 674 673 672 671 670 669 668 667 666 665 664 663 662 661 660 659 658 657 656 655 654 653 652 651 650 649 648 647 646 645 644 643 642 641 640 639 638 637 636 635 634 633 632 631 630 629 628 627 626 625 624 623 622 621 620 619 618 617 616 615 614 613 612 611 610 609 608 607 606 605 604 603 602 601 600 599 598 597 596 595 594 593 592 591 590 589 588 587 586 585 584 583 582 581 580 579 578 577 576 575 574 573 572 571 570 569 568 567 566 565 564 563 562 561 560 559 558 557 556 555 554 553 552 551 550 549 548 547 546 545 544 543 542 541 540 539 538 537 536 535 534 533 532 531 530 529 528 527 526 525 524 523 522 521 520 519 518 517 516 515 514 513 512 511 510 509 508 507 506 505 504 503 502 501 500 499 498 497 496 495 494 493 492 491 490 489 488 487 486 485 484 483 482 481 480 479 478 477 476 475 474 473 472 471 470 469 468 467 466 465 464 463 462 461 460 459 458 457 456 455 454 453 452 451 450 449 448 447 446 445 444 443 442 441 440 439 438 437 436 435 434 433 432 431 430 429 428 427 426 425 424 423 422 421 420 419 418 417 416 415 414 413 412 411 410 409 408 407 406 405 404 403 402 401 400 399 398 397 396 395 394 393 392 391 390 389 388 387 386 385 384 383 382 381 380 379 378 377 376 375 374 373 372 371 370 369 368 367 366 365 364 363 362 361 360 359 358 357 356 355 354 353 352 351 350 349 348 347 346 345 344 343 342 341 340 339 338 337 336 335 334 333 332 331 330 329 328 327 326 325 324 323 322 321 320 319 318 317 316 315 314 313 312 311 310 309 308 307 306 305 304 303 302 301 300 299 298 297 296 295 294 293 292 291 290 289 288 287 286 285 284 283 282 281 280 279 278 277 276 275 274 273 272 271 270 269 268 267 266 265 264 263 262 261 260 259 258 257 256 255 254 253 252 251 250 249 248 247 246 245 244 243 242 241 240 239 238 237 236 235 234 233 232 231 230 229 228 227 226 225 224 223 222 221 220 219 218 217 216 215 214 213 212 211 210 209 208 207 206 205 204 203 202 201 200 199 198 197 196 195 194 193 192 191 190 189 188 187 186 185 184 183 182 181 180 179 178 177 176 175 174 173 172 171 170 169 168 167 166 165 164 163 162 161 160 159 158 157 156 155 154 153 152 151 150 149 148 147 146 145 144 143 142 141 140 139 138 137 136 135 134 133 132 131 130 129 128 127 126 125 124 123 122 121 120 119 118 117 116 115 114 113 112 111 110 109 108 107 106 105 104 103 102 101 100 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

FIG. 6

LIN-56	MDHHAMYRTAEFNKTTVRLLAEFIEKGTGNATIVNMDSFLEFFAYLNPTA	50
	PIPTVPEIEKQLLKSPIRCIVCGMETESDSAVETSIDNASIILTATVIG	100
	YCRDPSDAVNOIRKESLRACIKHNSIFEHVIFEGLQIENTYCAHHAKYSL	150
	ANRWCKVYTMIRSSLGEQFTKFDVRNFKSILQSFLDTFGEIDDDKKDKES	200
	SHFDECFEEMDSENVEIKMESPQEEAAEKSKFSENLVEVKLEPIETHELD	250
	KTISDFSSDIIDSSQKLQNGFPEKVEQMDKYSNKLKDEASDKKYEKPG	300
	KKDYVEEEGYWAPITDSEDEA	322
69	RIVGMETESDSAVTLSIDNASTILTATVIGYCRDPSDAVNOIRKESLR	TKFNSIF
211	PIL EKALLMRESIAMTDNEAVKVLMAAVMSGHFRMATAEKATRHERRM	YDVDFVY
176	PIL I GNEVPGHR SIRVSDDDAALFETAAVLTDDQKTI RQAKRDDILSEYETV	LRSLHY
274	PILV INQQMEMTKVRSVNNTDAYIM IYVCVMNDKYDMDKAKELARMQRFKC	VS LDELY
		*
		*

FIG. 7

		10	20	30	40
	****
consensus	1	FDWEDYL---	EETGARAAPVELF---	DKQPVDSPPNGFKV	34
lin-61	146	VNYVNNCi-d	GEIVGQTSLSPKF---	DEGKALLSKHRFKV	181
lin-61	23	YLWESYLhqf	EKGKTSFIPVEAF---	NRNLTVPNFNECVKE	59
lin-61	388	FRWDEYL---	EKESAETLPLDLF---	KPMPSQERLDKFKV	421
hl(3)mbt	206	WSWESYL---	EEQKAITAPVSLFq---	DSQAVTHNKNKGFKL	240
hl(3)mbt	314	FSWSQYM---	CSTRAQAAPKHMf---	VSQSHSPPLGFQV	347
hl(3)mbt	422	FCWEKYL---	EETGASAVPTWAF-----	KVRPPHSFLV	451
tumor sup(Dm)	819	FRWSEYLk--	SGKDVAAPIHLf-----	LNPFPISPNCFEI	852
tumor sup(Dm)	926	FSWSRYL---	VKTGGKAAPRALFghl	NMQQMDVRNGFAV	962
tumor sup(Dm)	1035	FIWDDYI---	SEVGGMAASKELF-----	TPRQPMFYQE	1064
scmh1 (mouse)	28	FTWDKYL---	KETCSVPAPVHCF----	KQSYTPPSNEFKI	60
scml2 (human)	139	SSWPMFLl-k	TLNGSEMASATLf---	KKEPPKPPLNNFKV	174
		50	60	70	80
	****
consensus	35	-----GMKLEAVDP-----	RNPSLICVATVVEVKGYR	61	
lin-61	182	-----GQRLELLNY-----	SNSTEIRVARIQEICGRR	208	
lin-61	60	-----GVIFETVVHdydknc	DSIQVRWFARIEKVCGYR	92	
lin-61	422	iliskrvGLRLEAADM-----	CENQFICPATVKSVBGRL	455	
hl(3)mbt	241	-----GMKLEGIDP-----	QHPSMYFILTVAEVCGYR	267	
hl(3)mbt	348	-----GMKLEAVDR-----	MNPSLVCVASVTDVDSR	374	
hl(3)mbt	452	-----NMKLEAVDR-----	RNPALIRVASVEDVEDHR	478	
tumor sup(Dm)	853	-----GMKLEAIDP-----	ENCSLFCVCSSIVEVRGYR	879	
tumor sup(Dm)	963	-----GMHLEAEDL-----	NDTGKICVATVTDILDER	989	
tumor sup(Dm)	1065	-----RMKLEVVDQ-----	RNPCLIRPATVTRKGYR	1091	
scmh1 (mouse)	61	-----SMKLEAQDP-----	RNTTSTCIATVVGLTGAR	87	
scml2 (human)	175	-----GMKLEAIDK-----	KNPYLICPATIGDVKGDE	201	
		90	100	110	120
	****
consensus	62	LLLHFD-----	GWDDR-----	YDFWCDADSPDIF	85
lin-61	209	MNVSITkdkf	peslpdADDDRqvfssg	SQYWIDEGSFFIF	246
lin-61	93	VLAQFI-----	GAD-----	TKFWLNILSDDMF	114
lin-61	456	INVNFD-----	GWDEE-----	FDELYDVDSHDIL	479
hl(3)mbt	268	LRLHFD-----	GYSEC-----	HDFWVNANSPDIH	291
hl(3)mbt	375	FLVHFD-----	NWDDT-----	YDYWCDPSSPYIH	398
hl(3)mbt	479	IKIHFD-----	GWSHG-----	YDFWIDADHPDIH	502
tumor sup(Dm)	880	LKLSFD-----	GYSSM-----	YDFWVNADSQDIF	903
tumor sup(Dm)	990	IRVHFD-----	GWDDC-----	YDLWVHITSPYIH	1013
tumor sup(Dm)	1092	VQLHLD-----	CWPTD-----	YYFWLEDDSPDLH	1115
scmh1 (mouse)	88	LRLRLD-----	GSDNK-----	NDFWRLVDSSEIQ	111
scml2 (human)	202	VHITFD-----	GWSGA-----	FDYWCKYDSRDIF	225
		130			
	**		
consensus	86	PVGWCEKNGHPLQPP	100		
lin-61	249	PVGFAAVNGYQLNAK	263		
lin-61	115	GLANAAM-SDPNMDK	128		
lin-61	480	PIGWCEAHSYVLQPP	494		
hl(3)mbt	292	PAGWFEKTGHKLQLP	306		
hl(3)mbt	399	PVGWCQKQKPLTPP	413		
hl(3)mbt	503	PAGWCSKTGHPLQPP	517		
tumor sup(Dm)	904	PPGWCDATARVLQAP	918		
tumor sup(Dm)	1014	PCGWHEGRQQLIVPP	1028		
tumor sup(Dm)	1116	PIGWCEATSHELETP	1130		
scmh1 (mouse)	112	PIGNCEKNGGMLQPP	126		
scml2 (human)	226	PAGWCRLTGDVLQPP	240		

SCANNED, # 20

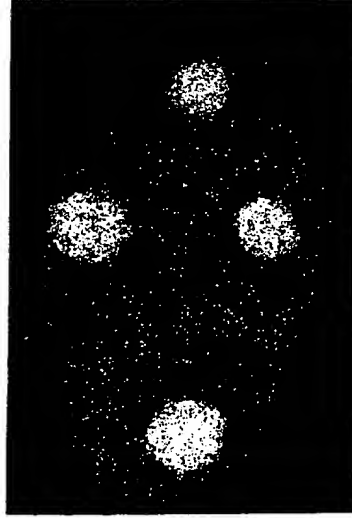
498
410
512

FIG. 9A



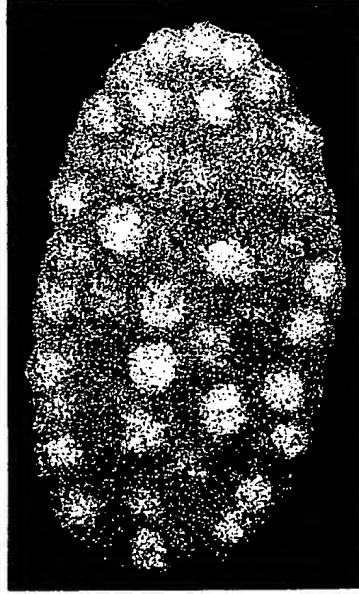
2-cell embryo

FIG. 9B



4-cell embryo

FIG. 9C



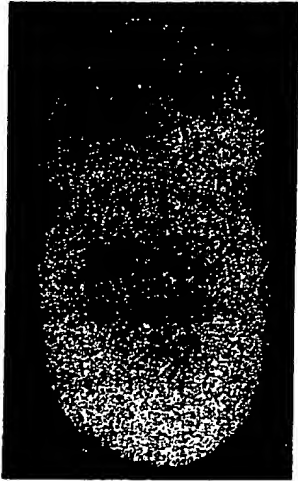
multicellular embryo

FIG. 9D



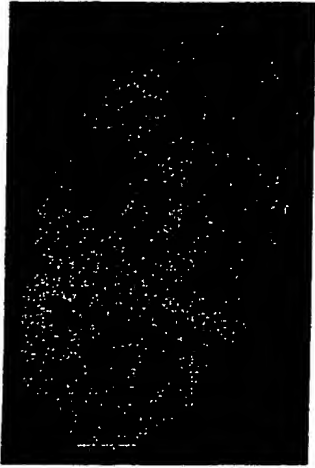
vulval region of an L4 larva

FIG. 10A



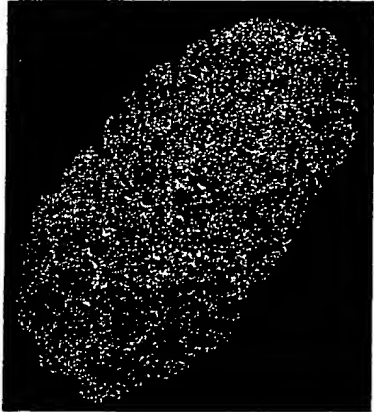
2-cell embryo

FIG. 10B



4-cell embryo

FIG. 10C



multicellular embryo

FIG. 10D



vulval region of an L4 larva

FIG.11A



FIG.11B

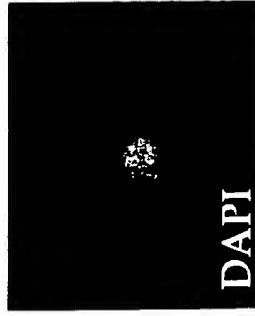
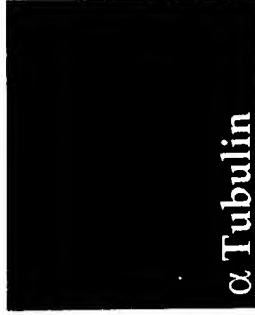


FIG.11C



DAPI

α Tubulin

FIG. 12A



FIG. 12B

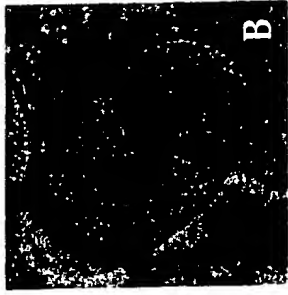


FIG. 12C



FIG. 12D



FIG. 12E

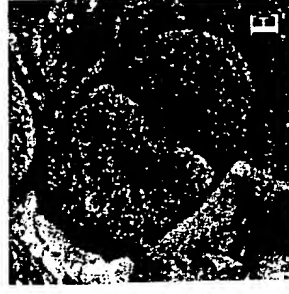


FIG. 12F

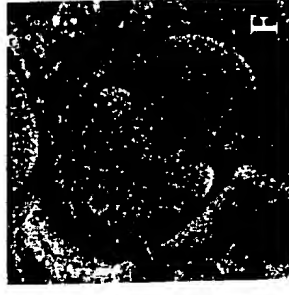


FIG. 12G



FIG. 12H



FIG. 13A

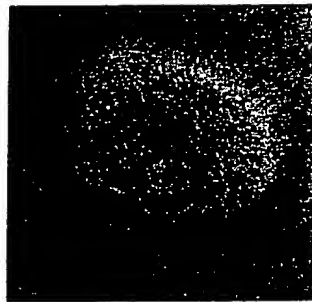


FIG. 13B

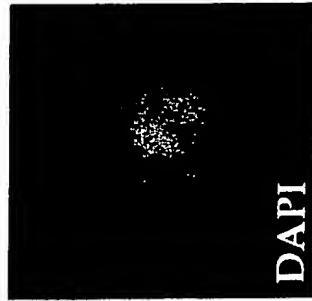


FIG. 13C

